

IN THE CLAIMS:

Please amend claims 4-13, 16, 19, 24-26, 29-32, 38, and 39 as follows:

4. (Amended) The potassium channel of Claim 3 wherein the pore-forming domain comprises SEQ ID NO:57, wherein
- (i) X at positions 1, 4, and 5 are T or S;
 - (ii) X at position 6 is I or V; and
 - (iii) X at position 8 is V, L, Y, F, M, or I.
5. (Amended) The potassium channel of Claim 4 where X at position 8 is L or I.
6. (Amended) The potassium channel of Claim 1, wherein at least one pore-forming domain is positioned proximal to an exterior portion of a cell membrane.
7. (Amended) The potassium channel of Claim 5 further comprising SEQ ID NO:58 downstream of said first pore-forming domain.
8. (Amended) The potassium channel of Claim 7 wherein SEQ ID NO:58 is positioned about 12-25 amino acids downstream of said first pore-forming domain.
9. (Amended) The potassium channel of Claim 8 wherein SEQ ID NO:58 is positioned within the second transmembrane domain.

FINNEGAN
HENDERSON
FARABOW
GARRETT &
DUNNER LLP

1300 I Street, NW
Washington, DC 20005
202.408.4000
Fax 202.408.4400
www.finnegan.com

10. (Amended) The potassium channel of Claim 8 wherein SEQ ID NO:58 is positioned beginning about 16 amino acids downstream of said first pore-forming domain.

11. (Amended) The potassium channel of Claim 8, wherein a second peptide comprising SEQ ID NO:58 is located within said second pore-forming region.

12. (Amended) The potassium channel of Claim 8, wherein X at positions 1-4 are the amino acids YALL.

13. (Amended) The potassium channel of Claim 12 wherein SEQ ID NO:58 is the amino acids YALLGIP.

16. (Amended) The potassium channel of Claim 1, characterized in that it is derived from invertebrates.

19. (Amended) The potassium channel of Claim 1, characterized in that it is derived from vertebrates.

24. (Amended) An isolated nucleotide sequence comprising
- (i) the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:36;
 - (ii) a nucleotide sequence that hybridizes to said sequence of SEQ ID NO:1 or SEQ ID NO:36;

ID NO:36;

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www.finnegan.com

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(iii) a nucleotide sequence that is degenerate to the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:36; or

(iv) a functional derivative of the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:36.

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25. (Amended) An isolated nucleotide sequence comprising

(i) the nucleotide sequence of SEQ ID NO:46;

(ii) a nucleotide sequence that hybridizes to said sequence of SEQ ID NO:46;

(iii) a nucleotide sequence that is degenerate to the nucleotide sequence of SEQ ID NO:46; or

(iv) a functional derivative of the nucleotide sequence of SEQ ID NO:46.

Eb Cont

26. (Amended) An isolated nucleotide sequence comprising

(i) the nucleotide sequence of SEQ ID NO:51, SEQ ID NO:52, or SEQ ID NO:53;

(ii) a nucleotide sequence that hybridizes to said sequence of SEQ ID NO:51, SEQ ID NO:52, or SEQ ID NO:53;

(iii) a nucleotide sequence that is degenerate to the nucleotide sequence of SEQ ID NO:51, SEQ ID NO:52, or SEQ ID NO:53; or

(iv) a functional derivative of the nucleotide sequence of SEQ ID NO:52, SEQ ID NO:52, or SEQ ID NO:53.

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29. (Amended) An expression vector capable of expressing the potassium channel encoded by the nucleotide sequence of Claim 24 in a cell membrane of a yeast cell.

30. (Amended) A transformed yeast cell comprising the expression vector of Claim 27.

31. (Amended) A method of assaying substances to determine effects on cell growth, the method comprising the steps of:

- a) preparing cultures of yeast cells in a medium adequate to support growth of potassium-dependent mutant strains expressing the nucleotide sequence of Claim 22;
- b) contacting said substance to a portion of said yeast cells thereafter permitting sufficient time for continued growth, if any, of the portion of yeast cells so contacted as well as the portion not contacted with said substance;
- c) identifying zones of growth around the substances, wherein the level of growth indicates whether or not activity of the heterologous potassium channel has been modulated as compared to yeast cells not contacted with said substances.

32. (Amended) The method of Claim 31 wherein said yeast cells comprise the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:36, SEQ ID NO:46, SEQ ID NO:51, SEQ ID NO:52, or SEQ ID NO:53.